

IN THE CLAIMS:

Please amend claims 1 and 34 as follows:

1. (Currently Amended) A compound comprising two or more antigen binding regions linked to at least one prodrug-activating enzyme, wherein

- a) the antigen binding regions consist of a single polypeptide chain;
- b) the single polypeptide chain is comprised of a first variable domain, a second variable domain, and a polypeptide linker connecting the first variable domain and the second variable domain; wherein a nucleotide sequence encoding the polypeptide linker is formed by two partially overlapping PCR primers during a PCR reaction that links the first variable domain and the second variable domain; and
wherein
- ~~e) a nucleotide sequence encoding the polypeptide linker is formed by two partially overlapping PCR primers during a PCR reaction that links the first variable domain and the second variable domain; and~~
wherein
- ~~d) c)~~ the compound has a bivalent or a multivalent structure.

2. (Previously Presented) A compound as claimed in claim 1, wherein the compound further comprises covalently bonded carbohydrates.

3. (Previously Presented) A compound as claimed in claim 1, wherein at least one antigen binding region comprises a variable domain of a heavy antibody chain and a variable domain of a light antibody chain (sFv fragment).

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4. (Original) A compound as claimed in claim 1, wherein the antigen binding region binds to a tumor-associated antigen (TAA).

5. (Previously Presented) A compound as claimed in claim 4, wherein the TAA is selected from the group consisting of an N-CAM, PEM, EGF-R, Sialyl-Le^a, Sialyl-Le^x, TF β , GICA, GD₃, GD₂, TAG72, CA125, the 24-25 kDa glycoprotein defined by Mab L6, and CEA.

6. (Previously Presented) A compound as claimed in claim 1, wherein the enzyme is selected from the group consisting of a lactamase, pyroglutamate aminopeptidase, D-aminopeptidase, oxidase, peroxidase, phosphatase, hydroxynitrile lyase, protease, esterase, carboxypeptidase and glycosidase.

7. (Previously Presented) A compound as claimed in claim 6, wherein the enzyme is a β -glucuronidase, which is selected from the group consisting of an *E. coli* β -glucuronidase, a *Kobayasia nipponica* β -glucuronidase, a *Secale cereale* β -glucuronidase and a human β -glucuronidase.

8. (Original) A compound as claimed in claim 1, wherein the antigen binding region is linked to the enzyme via a peptide linker.

9. (Previously Presented) A compound as claimed in claim 2, wherein glycosylation covalently bonds the carbohydrates to the compound, and the glycosylation takes place either by means of chemical methods or by a selection of suitable expression systems.

10. (Previously Presented) A compound as claimed in claim 1, which has undergone secretory expression in *Saccharomyces cerevisiae* or in *Hansenula polymorpha*.

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11. (Previously Presented) A compound as claimed in claim 1, which is expressed in *E. coli* and is subsequently chemically glycosylated.

12. (Previously Presented) A compound as claimed in claim 30, wherein the sFv- β -lactamase fusion protein has undergone periplasmic expression in *E. coli* and is chemically glycosylated.

13. (Previously Presented) A compound as claimed in claim 30, wherein the sFv- β -lactamase fusion protein has undergone secretory expression in *Saccharomyces cerevisiae* or *Hansenula polymorpha*.

14. (Withdrawn) A nucleic acid coding for a compound as claimed in claim 1.

15. (Withdrawn) A nucleic acid as claimed in claim 14, coding for a humanized sFv fragment against CEA and a human β -glucuronidase.

16. (Withdrawn) A nucleic acid as claimed in claim 14 with the sequence

CCAAGCTTAT GAATATGCAA ATCCTGCTCA TGAATATGCA AATCCTCTGA	50
ATCTACATGG TAAATATAGG TTTGTCTATA CCACAAACAG AAAAACATGA	100
GATCACAGTT CTCTCTACAG TTAGTGAGCA CACAGGACCT CACC ATG GGA TGG	153
AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGTAAGGGGC	199
Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr	
-10	
TCACAGTAGC AGGCTTGAGG TCTGGACATA TATATGGGTG ACAATAGACAT	249
CCACTTTGCC TTTCTCTCCA CA GGT GTC CAC TCC CAG GTC CAA CTG CAG	298
Gly Val His Ser Gln Val Gln Leu Gln	
1	
GAG AGC GGT CCA GGT CTT GTG AGA CCT AGC CAG ACC CTG AGC CTG	343
Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser Leu	
10	
ACC TGC ACC GTG TCT GGC TTC ACC ATC AGC AGT GGT TAT AGC TGG	388
Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly Tyr Ser Trp	
30	
CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT GAG TGG ATT GGA	433
His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly	
40	

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TAC ATA CAG TAC AGT GGT ATC ACT AAC TAC AAC CCC TCT CTC AAA 478
Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys
60
AGT AGA GTG ACA ATG CTG GTA GAC ACC AGC AAG AAC CAG TTC AGC 523
Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser
70 80
CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC TAT TAT 568
Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
90
TGT GCA AGA GAA GAC TAT GAT TAC CAC TGG TAC TTC GAT GTC TGG 613
Cys Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp
100 110
GGC CAA CCC ACC ACG GTC ACC GTC TCC TCA GGA GGC GGT GGA TCG 658
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
120
GGC GGT GGT GGG TCG GGT GGC GGC GGA TCT GAC ATC CAG CTG ACC 703
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 140
CAG AGC CCA AGC AGC CTG AGC GCC AGC CTC GGT GAC AGA GTG ACC 748
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
150
ATC ACC TGT AGT ACC AGC TCG AGT GTA AGT TAC ATG CAC TGG TAC 793
Ile Thr Cys Ser Thr Ser Ser Ser Val Ser Tyr Met His Trp Tyr
160 170
CAG CAG AAG CCA GGT AAG GCT CCA AAG CTG CTG ATC TAC AGC ACA 838
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Thr
180
TCC AAC CTG GCT TCT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT 883
Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
190 200
AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG 928
Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
210
GAC ATC GCC ACC TAC TAC TGC CAT CAG TGG AGT AGT TAT CCC ACG 973
Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser Ser Tyr Pro Thr
220 230
TTC GGC CAA GGG ACC AAG CTG GAG ATC AAA GGTGAGTAGA ATTTAACTTT 1023
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
240
TGCTTCCTCA GTTGGATCTG AGTAACTCCC AATCTTCTCT CTGCA GAG CTC AAA 1077
Glu Leu Lys
ACC CCA CTT GGT GAC ACA ACT CAC ACA TGC CCA CGG TGC CCA 1119
Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro
250
GGTAAGCCAG CCCAGGACTC GCCCTCCAGC TCAAGGCGGG ACAAGAGCCC 1169
TAGAGTGGCC TGAGTCCAGG GACAGGCCC AGCAGGGTGC TGACGCATCC 1219

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CTT TTG GAT GCA GAA AAC AAA GTC GTG GCG AAT GGG ACT GGG ACC	2036
Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr Gly Thr	
510	
CAG GGC CAA CTT AAG GTG CCA GGT GTC AGC CTC TGG TGG CCG TAC	2081
Gln Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro Tyr	
520 530	
CTG ATG CAC GAA CGC CCT GCC TAT CTG TAT TCA TTG GAG GTG CAG	2126
Leu Met His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu Val Gln	
540	
CTG ACT GCA CAG ACG TCA CTG GGG CCT GTG TCT GAC TTC TAC ACA	2171
Leu Thr Ala Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr	
550 560	
CTC CCT GTG GGG ATC CGC ACT GTG GCT GTC ACC AAG AGC CAG TTC	2216
Leu Pro Val Gly Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe	
570	
CTC ATC AAT GGG AAA CCT TTC TAT TTC CAC GGT GTC AAC AAG CAT	2261
Leu Ile Asn Gly Lys Pro Phe Tyr Phe His Gly Val Asn Lys His	
580 590	
GAG GAT GCG GAC ATC CGA GGG AAG GGC TTC GAC TGG CCG CTG CTG	2306
Glu Asp Ala Asp Ile Arg Gly Lys Gly Phe Asp Trp Pro Leu Leu	
600	
GTG AAG GAC TTC AAC CTG CTT CGC TGG CTT GGT GCC AAC GCT TTC	2351
Val Lys Asp Phe Asn Leu Leu Arg Trp Leu Gly Ala Asn Ala Phe	
610 620	
CGT ACC AGC CAC TAC CCC TAT GCA GAG GAA GTG ATG CAG ATG TGT	2396
Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu Val Met Gln Met Cys	
630	
GAC CGC TAT GGG ATT GTG GTC ATC GAT GAG TGT CCC GGC GTG GGC	2441
Asp Arg Tyr Gly Ile Val Val Ile Asp Glu Cys Pro Gly Val Gly	
640 650	
CTG GCG CTG CCG CAG TTC TTC AAC AAC GTT TCT CTG CAT CAC CAC	2486
Leu Ala Leu Pro Gln Phe Phe Asn Asn Val Ser Leu His His His	
660	
ATG CAG GTG ATG GAA GAA GTG GTG CGT AGG GAC AAG AAC CAC CCC	2531
Met Gln Val Met Glu Glu Val Val Arg Arg Asp Lys Asn His Pro	
670 680	
GCG GTC GTG ATG TGG TCT GTG GCC AAC GAG CCT GCG TCC CAC CTA	2576
Ala Val Val Met Trp Ser Val Ala Asn Glu Pro Ala Ser His Leu	
690	
GAA TCT GCT GGC TAC TAC TTG AAG ATG GTG ATC GCT CAC ACC AAA	2621
Glu Ser Ala Gly Tyr Tyr Leu Lys Met Val Ile Ala His Thr Lys	
700 710	
TCC TTG GAC CCC TCC CGG CCT GTG ACC TTT GTG AGC AAC TCT AAC	2666
Ser Leu Asp Pro Ser Arg Pro Val Thr Phe Val Ser Asn Ser Asn	
720	
TAT GCA GCA GAC AAG GGG GCT CCG TAT GTG GAT GTG ATC TGT TTG	2711
Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val Asp Val Ile Cys Leu	
730 740	
AAC AGC TAC TAC TCT TGG TAT CAC GAC TAC GGG CAC CTG GAG TTG	2756
Asn Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly His Leu Glu Leu	
750	

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ATT CAG CTG CAG CTG GCC ACC CAG TTT GAG AAC TGG TAT AAG AAG 2801
 Ile Gln Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp Tyr Lys Lys
 760 770
 TAT CAG AAG CCC ATT ATT CAG AGC GAG TAT GGA GCA GAA ACG ATT 2846
 Tyr Gln Lys Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu Thr Ile
 780
 GCA GGG TTT CAC CAG GAT CCA CCT CTG ATG TTC ACT GAA GAG TAC 2891
 Ala Gly Phe His Gln Asp Pro Pro Leu Met Phe Thr Glu Glu Tyr
 790 800
 CAG AAA AGT CTG CTA GAG CAG TAC CAT CTG GGT CTG GAT CAA AAA 2936
 Gln Lys Ser Leu Leu Glu Gln Tyr His Leu Gly Leu Asp Gln Lys
 810
 CGC AGA AAA TAT GTG GTT GGA GAG CTC ATT TGG AAT TTT GCC GAT 2981
 Arg Arg Lys Tyr Val Val Gly Glu Leu Ile Trp Asn Phe Ala Asp
 820 830
 TTC ATG ACT GAA CAG TCA CCG ACG AGA GTG CTG GGG ATT AAA AAG 3026
 Phe Met Thr Glu Gln Ser Pro Thr Arg Val Leu Gly Asn Lys Lys
 840
 GGG ATC TTC ACT CGG CAG AGA CAA CCA AAA AGT GCA GCG TTC CTT 3071
 Gly Ile Phe Thr Arg Gln Arg Gln Pro Lys Ser Ala Ala Phe Leu
 850 860
 TTG CGA GAG AGA TAC TGG AAG ATT GCC AAT GAA ACC AGG TAT CCC 3116
 Leu Arg Glu Arg Tyr Trp Lys Ile Ala Asn Glu Thr Arg Tyr Pro
 870
 CAC TCA GTA GCC AAG TCA CAA TGT TTG GAA AAC AGC CCG TTT ACT 3161
 His Ser Val Ala Lys Ser Gln Cys Leu Glu Asn Ser Pro Phe Thr
 880 890
 TGA GCAAGACTGA TACCACCTGC GTGTCCCTTC CTCCCCGAGT CAGGGCGACT 3214
 TCCACAGCAG CAGACAAGT GCCTCCTGGA CTGTTACGG CAGACCAGAA 3264
 CGTTTCTGGC CTGGGTTTTG TGGTCATCTA TTCTAGCAGG GAACACTAAA 3314.

17. (Withdrawn) A vector containing a nucleic acid as claimed in claim 14.

18. (Withdrawn) A host cell containing a nucleic acid as claimed in claim 14 or a vector as claimed in claim 17.

19. (Withdrawn) A host cell as claimed in claim 18, which is a BHK, CHO, COS, HeLa, insect, tobacco plant, yeast or *E. coli* cell.

20. (Withdrawn) A transgenic mammal with the exception of a human, containing a DNA as claimed in claim 14 or a vector as claimed in claim 17.

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21. (Withdrawn) A process for preparing a compound as claimed in claim 1, which comprises
- a) introducing a nucleic acid as claimed in claim 14 or a vector as claimed in claim 17 into a host cell,
 - b) cultivating the host cell, and
 - c) isolating the compound.
22. (Withdrawn) A process for preparing a compound as claimed in claim 1, which comprises
- a) cultivating a host cell as claimed in claim 18, and
 - b) isolating the compound.
23. (Canceled).
24. (Canceled).
25. (Previously Presented) A pharmaceutical composition comprising a compound as claimed in claim 1 and a physiologically acceptable carrier.
26. (Previously Presented) A diagnostic aid comprising a compound as claimed in claim 1.
27. (Previously Presented) A compound as claimed in claim 6, wherein the lactamase enzyme is a *Bacillus cereus* β -lactamase II.
28. (Previously Presented) A compound as claimed in claim 6, wherein the carboxypeptidase enzyme is a carboxypeptidase G2 from *Pseudomonas*.
29. (Previously Presented) A compound as claimed in claim 10, which has undergone secretory expression in *Hansenula polymorpha*.

30. (Previously Presented) A compound as claimed in claim 1, wherein at least one antigen binding region and at least one prodrug-activating enzyme form an sFv- β -lactamase fusion protein.

31. (Previously Presented) A compound as claimed in claim 11, wherein the chemical glycosylation involves at least one of galactosylation or mannosylation.

32. (Previously Presented) A compound as claimed in claim 12, wherein the chemical glycosylation involves at least one of galactosylation or mannosylation.

33. (Previously Presented) A method of treating cancer comprising administering a compound claimed in claim 1 to a host in need thereof and subsequently administering a prodrug to be activated by the enzyme portion of the compound of claim 1.

34. (Currently Amended) A compound comprising one or more antigen binding regions linked to at least one prodrug-activating enzyme, wherein

- a) the antigen binding regions consist of a single polypeptide chain;
- b) the single polypeptide chain is comprised of a first variable domain, a second variable domain, and a polypeptide linker connecting the first variable domain and the second variable domain; wherein a nucleotide sequence encoding the polypeptide linker is formed by two partially overlapping PCR primers during a PCR reaction that links the first variable domain and the second variable domain; and
wherein
- ~~c) a nucleotide sequence encoding the polypeptide linker is formed by two partially overlapping PCR primers during a PCR reaction that~~

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~~links the first variable domain and the second variable domain; and~~

wherein

d) c) the compound has a monovalent, bivalent, or multivalent structure.

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